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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/654,328

DATE: 09/20/2000
 TIME: 12:20:48

Input Set : A:\B08017187.txt
 Output Set: N:\CRF3\09202000\I654328.raw

4 <110> APPLICANT: Brenner, Michael B.
 5 Valencia, Xavier
 7 <120> TITLE OF INVENTION: Methods and Compositions for Treatment
 8 of Inflammatory Disease Using Cadherin-11 Modulating Agents
 11 <130> FILE REFERENCE: B0801/7187/ERP/MAT
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/654,328
 C--> 14 <141> CURRENT FILING DATE: 2000-09-01
 14 <150> PRIOR APPLICATION NUMBER: US 60/152,456
 16 <151> PRIOR FILING DATE: 1999-09-03
 18 <150> PRIOR APPLICATION NUMBER: US 60/153,490
 20 <151> PRIOR FILING DATE: 1999-09-13
 23 <160> NUMBER OF SEQ ID NOS: 12
 25 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 2625
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Homo Sapiens
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (156)...(2546)
 36 <400> SEQUENCE: 1
 37 cgcagccct gacgtatga gctcaaccag cagagacatt ccatccaaag agaggtctgc 60
 38 gtgacgcgtc cgggaggcca ccctcgacaa gaccacgtatgttgg aagggttgc 120
 39 agtcgcattc tccatgtgc accacgttaac caaaa atg aag gag aac tac tgt 173
 40 Met Lys Glu Asn Tyr Cys
 41 1 5
 43 tttaaaa gcc ggc ctg gtg tgc ctg ggc atg ctg tgc cac agc cat ggc 221
 44 Leu Gln Ala Ala Leu Val Cys Leu Gly Met Leu Cys His Ser His Ala
 45 10 15 20
 47 ttt gcc cca gag cgg cgg ggg cac ctg cgg ccc tcc ttc cat ggg cac 269
 48 Phe Ala Pro Glu Arg Arg Gly His Leu Arg Pro Ser Phe His Gly His
 49 25 30 35
 51 cat gag aag ggc aag gag ggg cag gtg cta cag cgc tcc aag cgt ggc 317
 52 His Glu Lys Gly Lys Glu Gly Gln Val Leu Gln Arg Ser Lys Arg Gly
 53 40 45 50
 55 tgg gtc tgg aac cag ttc ttc gtg ata gag gag tac acc ggg cct gac 365
 56 Trp Val Trp Asn Gln Phe Phe Val Ile Glu Glu Tyr Thr Gly Pro Asp
 57 55 60 65 70
 59 ccc gtg ctt gtg ggc agg ctt cat tca gat att gac tct ggt gat ggg 413
 60 Pro Val Leu Val Gly Arg Leu His Ser Asp Ile Asp Ser Gly Asp Gly
 61 75 80 85
 63 aac att aaa tac att ctc tca ggg gaa gga gtc gga acc att ttt gtg 461
 64 Asn Ile Lys Tyr Ile Leu Ser Gly Glu Gly Ala Gly Thr Ile Phe Val
 65 90 95 100
 67 att gat gac aaa tca ggg aac att cat gcc acc aag acg ttg gat cga 509
 68 Ile Asp Asp Lys Ser Gly Asn Ile His Ala Thr Lys Thr Leu Asp Arg
 69 105 110 115

ENTERED

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| | | |
|-----|---|------|
| 71 | gaa gag aga gcc cag tac acg ttg atg gct cag gcg gtg gac agg gac | 557 |
| 72 | Glu Glu Arg Ala Gln Tyr Thr Leu Met Ala Gln Ala Val Asp Arg Asp | |
| 73 | 120 125 130 | |
| 75 | acc aat cgg cca ctg gag cca ccg tcg gaa ttc att gtc aag gtc cag | 605 |
| 76 | Thr Asn Arg Pro Leu Glu Pro Pro Ser Glu Phe Ile Val Lys Val Gln | |
| 77 | 135 140 145 150 | |
| 79 | gac att aat gac aac cct ccg gag ttc ctg cac gag acc tat cat gcc | 653 |
| 80 | Asp Ile Asn Asp Asn Pro Pro Glu Phe Leu His Glu Thr Tyr His Ala | |
| 81 | 155 160 165 | |
| 83 | aac gtg cct gag agg tcc aat gtg gga acg tca gta atc cag gtg aca | 701 |
| 84 | Asn Val Pro Glu Arg Ser Asn Val Gly Thr Ser Val Ile Gln Val Thr | |
| 85 | 170 175 180 | |
| 87 | gct tca gat gca gat gac ccc act tat gga aat agc gcc aag tta gtg | 749 |
| 88 | Ala Ser Asp Ala Asp Asp Pro Thr Tyr Gly Asn Ser Ala Lys Leu Val | |
| 89 | 185 190 195 | |
| 91 | tac agt ctc gaa gga caa ccc tat ttt tcg gtg gaa gca cag aca | 797 |
| 92 | Tyr Ser Ile Leu Glu Gly Gin Pro Tyr Phe Ser Val Glu Ala Gln Thr | |
| 93 | 200 205 210 | |
| 95 | ggt atc atc aga aca gcc cta ccc aac atg gac agg gag gcc aag gag | 845 |
| 96 | Gly Ile Ile Arg Thr Ala Leu Pro Asn Met Asp Arg Glu Ala Lys Glu | |
| 97 | 215 220 225 230 | |
| 99 | gag tac cac gtg gtg atc cag gcc aag gac atg ggt gga cat atg ggc | 893 |
| 100 | Glu Tyr His Val Val Ile Gln Ala Lys Asp Met Gly Gly His Met Gly | |
| 101 | 235 240 245 | |
| 103 | gga ctc tca ggg aca acc aaa gtg acg atc aca ctg acc gat gtc aat | 941 |
| 104 | Gly Leu Ser Gly Thr Thr Lys Val Thr Ile Thr Leu Thr Asp Val Asn | |
| 105 | 250 255 260 | |
| 107 | gac aac cca cca aag ttt ccg cag agg cta tac cag atg tct gtg tca | 989 |
| 108 | Asp Asn Pro Pro Lys Phe Pro Gln Arg Leu Tyr Gln Met Ser Val Ser | |
| 109 | 265 270 275 | |
| 111 | gaa gca gcc gtc cct ggg gag gaa gta gga aga gtg aaa gct aaa gat | 1037 |
| 112 | Glu Ala Ala Val Pro Gly Glu Glu Val Gly Arg Val Lys Ala Lys Asp | |
| 113 | 280 285 290 | |
| 115 | cca gac att gga gaa aat ggc tta gtc aca tac aat att gtt gat gga | 1085 |
| 116 | Pro Asp Ile Gly Glu Asn Gly Leu Val Thr Tyr Asn Ile Val Asp Gly | |
| 117 | 295 300 305 310 | |
| 119 | gat ggt atg gaa tcg ttt gaa atc aca acg gac tat gaa aca cag gag | 1133 |
| 120 | Asp Gly Met Glu Ser Phe Glu Ile Thr Thr Asp Tyr Glu Thr Gln Glu | |
| 121 | 315 320 325 | |
| 123 | ggg gtg ata aag ctg aaa aag cct gta gat ttt gaa acc gaa aga gcc | 1181 |
| 124 | Gly Val Ile Lys Leu Lys Lys Pro Val Asp Phe Glu Thr Glu Arg Ala | |
| 125 | 330 335 340 | |
| 127 | tat agc ttg aag gta gag gca gcc aac gtg cac atc gac ccg aag ttt | 1229 |
| 128 | Tyr Ser Leu Lys Val Glu Ala Ala Asn Val His Ile Asp Pro Lys Phe | |
| 129 | 345 350 355 | |
| 131 | atc agc aat ggc cct ttc aag gac act gtg acc gtc aag atc tca gta | 1277 |
| 132 | Ile Ser Asn Gly Pro Phe Lys Asp Thr Val Thr Val Lys Ile Ser Val | |
| 133 | 360 365 370 | |
| 135 | gaa gat gct gat gag ccc cct atg ttc ttg gcc cca agt tac atc cac | 1325 |

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| | | |
|-----|---|------|
| 136 | Glu Asp Ala Asp Glu Pro Pro Met Phe Leu Ala Pro Ser Tyr Ile His | |
| 137 | 375 380 385 390 | |
| 139 | gaa gtc caa gaa aat gca gct gct ggc acc gtg gtt ggg aga gtc cat | 1373 |
| 140 | Glu Val Gln Glu Asn Ala Ala Gly Thr Val Val Gly Arg Val His | |
| 141 | 395 400 405 | |
| 143 | gcc aaa gac cct gat gtc aac agc ccg ata agg tat tcc atc gat | 1421 |
| 144 | Ala Lys Asp Pro Asp Ala Ala Asn Ser Pro Ile Arg Tyr Ser Ile Asp | |
| 145 | 410 415 420 | |
| 147 | cgt cac act gac ctc gac aga ttt ttc act att aat cca gag gat ggt | 1469 |
| 148 | Arg His Thr Asp Leu Asp Arg Phe Phe Thr Ile Asn Pro Glu Asp Gly | |
| 149 | 425 430 435 | |
| 151 | ttt att aaa act aca aaa cct ctg gat aga gag gaa aca gca gcc tgg ctc | 1517 |
| 152 | Phe Ile Lys Thr Thr Lys Pro Leu Asp Arg Glu Glu Thr Ala Trp Leu | |
| 153 | 440 445 450 | |
| 155 | aac atc act gtc ttt gca gca gaa atc cac aat ccg cat cag gaa gcc | 1565 |
| 156 | Asn Ile Thr Val Phe Ala Ala Glu Ile His Asn Arg His Gln Glu Ala | |
| 157 | 455 460 465 470 | |
| 159 | caa gtc cca gtg gcc att agg gtc ctt gat gtc aac gat aat gct ccc | 1613 |
| 160 | Gln Val Pro Val Ala Ile Arg Val Leu Asp Val Asn Asp Asn Ala Pro | |
| 161 | 475 480 485 | |
| 163 | aag ttt gct gcc cct tat gaa ggt ttc atc tgt gag agt gat cag acc | 1661 |
| 164 | Lys Phe Ala Ala Pro Tyr Glu Gly Phe Ile Cys Glu Ser Asp Gln Thr | |
| 165 | 490 495 500 | |
| 167 | aag cca ctt tcc aac cag cca att gtt aca att agt gca gat gac aag | 1709 |
| 168 | Lys Pro Leu Ser Asn Gln Pro Ile Val Thr Ile Ser Ala Asp Asp Lys | |
| 169 | 505 510 515 | |
| 171 | gat gac acg gcc aat gga cca aga ttt atc ttc agc cta ccc cct gaa | 1757 |
| 172 | Asp Asp Thr Ala Asn Gly Pro Arg Phe Ile Phe Ser Leu Pro Pro Glu | |
| 173 | 520 525 530 | |
| 175 | atc att cac aat cca aat ttc aca gtc aga gac aac cga gat aac aca | 1805 |
| 176 | Ile Ile His Asn Pro Asn Phe Thr Val Arg Asp Asn Arg Asp Asn Thr | |
| 177 | 535 540 545 550 | |
| 179 | gca ggc gtg tac gcc cgg cgt gga ggg ttc agt cgg cag aag cag gac | 1853 |
| 180 | Ala Gly Val Tyr Ala Arg Arg Gly Gly Phe Ser Arg Gln Lys Gln Asp | |
| 181 | 555 560 565 | |
| 183 | ttg tac ctt ctg ccc ata gtg atc agc gat ggc ggc atc ccg ccc atg | 1901 |
| 184 | Leu Tyr Leu Leu Pro Ile Val Ile Ser Asp Gly Gly Ile Pro Pro Met | |
| 185 | 570 575 580 | |
| 187 | agt agc acc aac acc ctc acc atc aaa gtc tgc ggg tgc gac gtg aac | 1949 |
| 188 | Ser Ser Thr Asn Thr Leu Thr Ile Lys Val Cys Gly Cys Asp Val Asn | |
| 189 | 585 590 595 | |
| 191 | ggg gca ctg ctc tcc tgc aac gca gag gcc tac att ctg aac gcc ggc | 1997 |
| 192 | Gly Ala Leu Leu Ser Cys Asn Ala Glu Ala Tyr Ile Leu Asn Ala Gly | |
| 193 | 600 605 610 | |
| 195 | ctg agc aca ggc gcc ctg atc gcc atc ctc gcc tgc atc gtc att ctc | 2045 |
| 196 | Leu Ser Thr Gly Ala Leu Ile Ala Ile Leu Ala Cys Ile Val Ile Leu | |
| 197 | 615 620 625 630 | |
| 199 | ctg gtc att gta gta ttg ttt gtg acc ctg aga agg caa aag aaa gaa | 2093 |
| 200 | Leu Val Ile Val Val Leu Phe Val Thr Leu Arg Arg Gln Lys Lys Glu | |

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| | | | | |
|-----|---|-----|-----|------|
| 201 | 635 | 640 | 645 | |
| 203 | cca ctc att gtc ttt gag gaa gaa gat gtc cgt gag aac atc att act | | | 2141 |
| 204 | Pro Leu Ile Val Phe Glu Glu Glu Asp Val Arg Glu Asn Ile Ile Thr | | | |
| 205 | 650 | 655 | 660 | |
| 207 | tat gat gat gaa ggg ggt ggg gaa gaa gac aca gaa gcc ttt gat att | | | 2189 |
| 208 | Tyr Asp Asp Glu Gly Gly Gly Glu Asp Thr Glu Ala Phe Asp Ile | | | |
| 209 | 665 | 670 | 675 | |
| 211 | gcc acc ctc cag aat cct gat ggt atc aat gga ttt atc ccc cgc aaa | | | 2237 |
| 212 | Ala Thr Leu Gln Asn Pro Asp Gly Ile Asn Gly Ile Pro Arg Lys | | | |
| 213 | 680 | 685 | 690 | |
| 215 | gac atc aaa cct gag tat cag tac atg cct aga cct ggg ctc cgg cca | | | 2285 |
| 216 | Asp Ile Lys Pro Glu Tyr Glu Tyr Met Pro Arg Pro Gly Leu Arg Pro | | | |
| 217 | 695 | 700 | 705 | 710 |
| 219 | gcg ccc aac agc gtg gat gtc gat gac ttc atc aac acg aga ata cag | | | 2333 |
| 220 | Ala Pro Asn Ser Val Asp Val Asp Asp Phe Ile Asn Thr Arg Ile Gln | | | |
| 221 | 715 | 720 | 725 | |
| 223 | gag gca gac aat gac ccc acg gct cct cct tat gac tcc att caa atc | | | 2381 |
| 224 | Glu Ala Asp Asn Asp Pro Thr Ala Pro Pro Tyr Asp Ser Ile Gln Ile | | | |
| 225 | 730 | 735 | 740 | |
| 227 | tac ggt tat gaa ggc agg ggc tca gtg gcc ggg tcc ctg agc tcc cta | | | 2429 |
| 228 | Tyr Gly Tyr Glu Gly Arg Gly Ser Val Ala Gly Ser Leu Ser Ser Leu | | | |
| 229 | 745 | 750 | 755 | |
| 231 | gag tcg gcc acc aca gat tca gac ttg gac tat gat tat cta cag aac | | | 2477 |
| 232 | Glu Ser Ala Thr Thr Asp Ser Asp Leu Asp Tyr Asp Tyr Leu Gln Asn | | | |
| 233 | 760 | 765 | 770 | |
| 235 | tgg gga cct cgt ttt aag aaa cta gca gat ttg tat ggt tcc aaa gac | | | 2525 |
| 236 | Trp Gly Pro Arg Phe Iys Lys Leu Ala Asp Leu Tyr Gly Ser Lys Asp | | | |
| 237 | 775 | 780 | 785 | 790 |
| 239 | act ttt gat gac gat tct taa caataacgat acaaatttgg ccttaagaac | | | 2576 |
| 240 | Thr Phe Asp Asp Asp Ser * | | | |
| 241 | 795 | | | |
| 243 | tgtgtctggc gttctcaaga atctagaaga tgtgttaacag gtatTTTT | | | 2625 |
| 245 | <210> SEQ ID NO: 2 | | | |
| 246 | <211> LENGTH: 796 | | | |
| 247 | <212> TYPE: PRT | | | |
| 248 | <213> ORGANISM: Homo Sapiens | | | |
| 250 | <400> SEQUENCE: 2 | | | |
| 251 | Met Lys Glu Asn Tyr Cys Leu Gln Ala Ala Leu Val Cys Leu Gly Met | | | |
| 252 | 1 | 5 | 10 | 15 |
| 253 | Leu Cys His Ser His Ala Phe Ala Pro Glu Arg Arg Gly His Leu Arg | | | |
| 254 | 20 | 25 | 30 | |
| 255 | Pro Ser Phe His Gly His His Glu Lys Gly Lys Glu Gly Gin Val Leu | | | |
| 256 | 35 | 40 | 45 | |
| 257 | Gln Arg Ser Lys Arg Gly Trp Val Trp Asn Gln Phe Phe Val Ile Glu | | | |
| 258 | 50 | 55 | 60 | |
| 259 | Glu Tyr Thr Gly Pro Asp Pro Val Leu Val Gly Arg Leu His Ser Asp | | | |
| 260 | 65 | 70 | 75 | 80 |
| 261 | Ile Asp Ser Gly Asp Gly Asn Ile Lys Tyr Ile Leu Ser Gly Glu Gly | | | |
| 262 | 85 | 90 | 95 | |

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263 Ala Gly Thr Ile Phe Val Ile Asp Asp Lys Ser Gly Asn Ile His Ala
264 100 105 110
265 Thr Lys Thr Leu Asp Arg Glu Glu Arg Ala Gln Tyr Thr Leu Met Ala
266 115 120 125
267 Gln Ala Val Asp Arg Asp Thr Asn Arg Pro Leu Glu Pro Pro Ser Glu
268 130 135 140
269 Phe Ile Val Lys Val Gln Asp Ile Asn Asp Asn Pro Pro Glu Phe Leu
270 145 150 155 160
271 His Glu Thr Tyr His Ala Asn Val Pro Glu Arg Ser Asn Val Gly Thr
272 165 170 175
273 Ser Val Ile Gln Val Thr Ala Ser Asp Ala Asp Asp Pro Thr Tyr Gly
274 180 185 190
275 Asn Ser Ala Lys Leu Val Tyr Ser Ile Leu Glu Gly Gln Pro Tyr Phe
276 195 200 205
277 Ser Val Glu Ala Gln Thr Gly Ile Ile Arg Thr Ala Leu Pro Asn Met
278 210 215 220
279 Asp Arg Glu Ala Lys Glu Glu Tyr His Val Val Ile Gln Ala Lys Asp
280 225 230 235 240
281 Met Gly Gly His Met Gly Gly Leu Ser Gly Thr Thr Lys Val Thr Ile
282 245 250 255
283 Thr Leu Thr Asp Val Asn Asp Asn Pro Pro Lys Phe Pro Gln Arg Leu
284 260 265 270
285 Tyr Gln Met Ser Val Ser Glu Ala Ala Val Pro Gly Glu Val Gly
286 275 280 285
287 Arg Val Lys Ala Lys Asp Pro Asp Ile Gly Glu Asn Gly Leu Val Thr
288 290 295 300
289 Tyr Asn Ile Val Asp Gly Asp Gly Met Glu Ser Phe Glu Ile Thr Thr
290 305 310 315 320
291 Asp Tyr Glu Thr Gln Glu Gly Val Ile Lys Leu Lys Lys Pro Val Asp
292 325 330 335
293 Phe Glu Thr Glu Arg Ala Tyr Ser Leu Lys Val Glu Ala Ala Asn Val
294 340 345 350
295 His Ile Asp Pro Lys Phe Ile Ser Asn Gly Pro Phe Lys Asp Thr Val
296 355 360 365
297 Thr Val Lys Ile Ser Val Glu Asp Ala Asp Glu Pro Pro Met Phe Leu
298 370 375 380
299 Ala Pro Ser Tyr Ile His Glu Val Gln Glu Asn Ala Ala Ala Gly Thr
300 385 390 395 400
301 Val Val Gly Arg Val His Ala Lys Asp Pro Asp Ala Ala Asn Ser Pro
302 405 410 415
303 Ile Arg Tyr Ser Ile Asp Arg His Thr Asp Leu Asp Arg Phe Phe Thr
304 420 425 430
305 Ile Asn Pro Glu Asp Gly Phe Ile Lys Thr Thr Lys Pro Leu Asp Arg
306 435 440 445
307 Glu Glu Thr Ala Trp Leu Asn Ile Thr Val Phe Ala Ala Glu Ile His
308 450 455 460
309 Asn Arg His Gln Glu Ala Gln Val Pro Val Ala Ile Arg Val Leu Asp
310 465 470 475 480
311 Val Asn Asp Asn Ala Pro Lys Phe Ala Ala Pro Tyr Glu Gly Phe Ile

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:411 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8